

#14



1600

TECH CENTER 1600/2900

MAY 15 2003

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DATE: 05/07/2003
TIME: 13:58:19RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/900,237AInput Set : A:\BB-1170USCIP-1.txt
Output Set: N:\CRF4\05072003\I900237A.raw

3 <110> APPLICANT: Allen, Stephen M.
 5 <120> TITLE OF INVENTION: Plant Cellulose Synthases
 7 <130> FILE REFERENCE: BB1170 US CIP
 9 <140> CURRENT APPLICATION NUMBER: US 09/900,237A
 10 <141> CURRENT FILING DATE: 2001-07-06
 12 <150> PRIOR APPLICATION NUMBER: US 60/092,844
 13 <151> PRIOR FILING DATE: 1998-07-14
 15 <150> PRIOR APPLICATION NUMBER: PCT/US99/15871
 16 <151> PRIOR FILING DATE: 1999-07-13
 18 <150> PRIOR APPLICATION NUMBER: 09/720383
 19 <151> PRIOR FILING DATE: 2000-12-21
 21 <160> NUMBER OF SEQ ID NOS: 33
 23 <170> SOFTWARE: Microsoft Office 97
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1221
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Hordeum vulgare
 30 <400> SEQUENCE: 1
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 32 catgccacca cgaccgttgtt tcaagggttc tgccccaatc aatctctctg accgtctcaa 120
 33 tcaagttctc cgggtggctc ttgggtcaat tgaaattctg tttagcagac attgtcctat 180
 34 ctggtaaat tacgtgggc ggttggaaact tctggagagg atggcttaca tcaacaccat 240
 35 tggtttatcca ataacatccc ttccacttat cgcctattgt gtgcttccctg ctatctgtct 300
 36 cctcaccaac aaatttatca ttcccgagat cagtaactat gctggatgt tctttattct 360
 37 tatgtttgcc tccatctttg ccacggat attggagctg cgtggatgt gtgtcggcat 420
 38 cgaggactgg tggagaaaacg agcagttctg ggttattgtt ggcacatctg cccatcttt 480
 39 cgcagtgttc cagggtctgc tgaagggttt ggccgggatt gacaccaact tcacggtac 540
 40 ctcgaaggca aacgacgagg atggcgatt tgctgagttt tacgtgttca agtggaccag 600
 41 tctcctcatt cctccgacca ccgtccttgc gattaacctg gtggcatgg tggcaggcat 660
 42 atcatatgcc atcaacagcg gttaccatgc ttgggttcca ctcttcggaa agctttctt 720
 43 ctcaatctgg gtgatcccttcc atctctaccc cttccctcaag ggtctcatgg ggaaggcagaa 780
 44 ccgcacgcca accatcgatca ttgtttggtc catccctcta gcctccatct tctccctcct 840
 45 gtgggtgaag atcgaccctt tcataatccga taccggaaa gccgtcgcca tggggcagtg 900
 46 tggcgtcaac tgctgatcggtt cggccgaagag tatctggcccc cctcgtgtaa ataccggagg 960
 47 ggggtggatg ggattttgtt gttgttagatg aagacggagt ttatgttaag ttattattgc 1020
 48 cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctcgtcggt acattgttat 1080
 49 ttttttctcc ttttcttcc atctgtgata cctgtgttt cttcttagag tatattatgt 1140
 50 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcaagctgt 1200
 51 tgcataact cttctgcaaa a 1221
 53 <210> SEQ ID NO: 2
 54 <211> LENGTH: 304
 55 <212> TYPE: PRT
 56 <213> ORGANISM: Hordeum vulgare

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58 <400> SEQUENCE: 2
 59 His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile
 60 1 5 10 15
 62 Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro
 63 20 25 30
 65 Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
 66 35 40 45
 68 Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
 69 50 55 60
 71 Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
 72 65 70 75 80
 74 Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
 75 85 90 95
 77 Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
 78 100 105 110
 80 Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
 81 115 120 125
 83 Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
 84 130 135 140
 86 Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
 87 145 150 155 160
 89 Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
 90 165 170 175
 92 Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
 93 180 185 190
 95 Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
 96 195 200 205
 98 Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
 99 210 215 220
 101 Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
 102 225 230 235 240
 104 Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
 105 245 250 255
 107 Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
 108 260 265 270
 110 Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
 111 275 280 285
 113 Ser Asp Thr Gln Lys Ala Val Ala Met Gly Gln Cys Gly Val Asn Cys
 114 290 295 300
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 117 <211> LENGTH: 3776
 118 <212> TYPE: DNA
 119 <213> ORGANISM: Zea mays
 121 <400> SEQUENCE: 3
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 123 aagcgtgtcc ctccccctcc ctcactccc tttcattcca ttccccccca gacgccgcta 120
 124 cccgcgcgcg cgcacgcacg cttgccccgg gatctggaga tctggtagcg ccagggggat 180
 125 ggaggccagc gccgggctgg tcgccccgtc gcacaaccgg aacgagctcg tcgtcatccg 240
 126 cgcgcatggc gagccaggc cgaagccat ggaccagcgg aacggccagg tgtgccagat 300

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127 ttgcggcgtac	gacgtggggc	gcaaccccgaa	cggggagccg	ttcgtggcct	gcaacgagtg	360
128 cgcctcccc	atctgcccgg	actgctacga	gtacgagcgc	cgcgagggca	cgcagaactg	420
129 cccccagtgc	aagaccggct	tcaagcgct	caaggggtgc	gcgcgcgtgc	ccggggacgaa	480
130 ggaggaggac	ggcgtcgacg	acctggagaa	cgagttcaac	tggagcaca	agcacgactc	540
131 ccagtaccc	gccgagtc	tgctccacgc	ccacatgagc	tacggccgcg	gcgcgcacct	600
132 cgacggcgtg	ccgcagccat	tccaccccat	ccccaatgtt	ccctccctca	ccaacggaca	660
133 gatggtcgtat	gacatcccgc	cggaccagca	cgcccttgtg	ccctcggtcg	tgggtggcgg	720
134 ggggaagagg	attcaccctc	tcccgtacgc	ggatccaaac	cttcctgtgc	aaccgagggtc	780
135 tatggaccct	tccaaggatc	tcgcccata	tggctacggg	agcgtagcat	ggaaggagag	840
136 gatggagagc	tggaagcaga	agcaggagag	gatgcaccag	acgaggaacg	atggcggcgg	900
137 cgatgtatgtt	gatgtatgcag	atctaccact	aatggatgaa	gctagacagc	cattgtccag	960
138 aaagatcccg	cttcctcaa	gccaaatcaa	cccctatagg	atgattataa	taattcggt	1020
139 agtggttttg	tgtttcttct	tccactaccg	agtgatgcat	ccgggtgcctg	atgcatttgc	1080
140 tttatggctc	atatctgtga	tctgtgaaat	ttgggttgc	atgtcttgg	ttcttgacca	1140
141 gtttccaaag	tggttccta	tcgagagggaa	aacctatctt	gaccggotga	gtttaagggtt	1200
142 tgacaaggaa	gggcattcctt	ctcaactcgc	ccctgttgc	ttctttgtca	gtacgggtga	1260
143 tcccttgaag	gaacccat	tggtactgc	taatactgtt	ctatctatcc	tttcgggtgga	1320
144 ttatccagg	gataagggtt	catgctacgt	ttctgtatgt	ggtgctgcca	tgctgacatt	1380
145 tgaaggattt	tctgaaacat	ctgaatttgc	aaagaaatgg	gttccttct	gcaaaagata	1440
146 tagcctttag	cctcgctc	cagagtggta	cttccaacag	aagatagact	acctgaaaga	1500
147 caaggtggcg	ccaaactttg	tttagagaacg	gagacaatg	aagagagagt	atgaggaatt	1560
148 caaggtcaga	atcaatgcct	tggttgctaa	agccaaaag	gttcctgagg	aaggatggac	1620
149 aatgcaggat	ggaactccat	ggcccgaaaa	taatgtccgt	gatcatctg	gaatgattca	1680
150 gttttcctt	ggtcaaagtg	gtggccatga	tgtggaaagga	aatgagctgc	ctcgattgg	1740
151 ttatgtttca	agagaaaaac	ggccaggct	caaccatcac	aagaaggctg	gtgctatgaa	1800
152 tgcattggtc	cgagtctctg	ctgtactaac	taatgtctct	tatttgctga	acttggattg	1860
153 tgatcactat	atcaataata	gtaaggctat	aaaggaagca	atgtgttta	tgatggatcc	1920
154 ttgcttggaa	aagaaagttt	gctatgtca	gtttcctcaa	agatttgatg	ggattgatcg	1980
155 ccatgatcga	tatgctaaca	gaaatgttgt	cttttcgat	atcaacatga	aaggtttgga	2040
156 tggtatccag	ggcccaattt	atgtgggtac	tggatgtgc	ttcagaaggc	aggcattata	2100
157 tggctacgat	gctcccaaaa	caaagaagcc	accatcaaga	acttgcaact	gctggccaaa	2160
158 gtggtgatt	tgctgttgct	gtttggtaa	caggaagacc	aagaagaaga	ccaagacctc	2220
159 taaaacctaaa	tttgagaaga	taaagaaact	tttaagaaa	aaggaaaatc	aagccctgc	2280
160 atatgcttt	ggtgaaattt	atgaagccgc	tccaggagct	gaaaatgaaa	aggctagtat	2340
161 tggtaaatcaa	cagaagttgg	aaaagaaatt	tggccagtct	tcagttttg	ttgcatccac	2400
162 acttctttag	aatggtgaa	ccctgaagag	tgccagtcca	gcttcttcc	tgaaggaagc	2460
163 tatacatgtc	atcagttgtg	gatatgaaga	caaaacaggc	tggggaaaag	atattggtt	2520
164 gatttatgga	tcagtcacag	aagatattct	tactggttt	aagatgcact	gccatggtt	2580
165 gcggtaatt	tactgcatac	ctaaacgggc	cgccttcaaa	ggttccgcac	ctctcaatct	2640
166 ttccgatctgt	cttcaccagg	ttcttcggtg	ggcttcttggt	tcaattgaaa	ttttcttcag	2700
167 caaccactgc	cctctcttgtt	atgggtatgg	tggtgacta	aagttcttgg	aaaggtttcc	2760
168 gtacattaaac	tccatcgat	acccttggac	atctatcccg	ctcttggcct	attgcacatt	2820
169 gcctgcccatt	tgcttgctga	cagggaaatt	tatcacgcca	gagcttaaca	atgttgccag	2880
170 cctctggttc	atgtcacttt	tcatctgc	ttttgtacgt	agcatcttgg	aatagagatg	2940
171 gagttgggtga	ggcatcgatg	actggtgag	aaacgagcag	ttttgggtca	ttggaggcgt	3000
172 gtcttcacat	ctctttgtg	tgttccagg	actcctcaag	gtcatagctg	gttagacac	3060
173 gagtttcact	gtgacatcca	aggcgggaga	cgacgaggag	ttctcagagc	tgtacacatt	3120
174 caaatggacg	acccttctga	tacctccgac	aaccctgctc	ctactgaact	tcattggagt	3180
175 gtagctgat	atctccaatg	cgatcaacaa	cggatatgaa	tcatggggcc	ccctgttcgg	3240

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176 gaagctcttc tttgcattt gggtgatcg ccatcttac ccgtcctca agggcttggt 3300
 177 tgggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
 178 cttctcgctg ctggggtcc ggatcgaccc gttccttgcg aaggatgatg gtcccctgtt 3420
 179 ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480
 180 tggtcgaaga agtattttt cagatgtttt gtgcccatat ttctttttc aattttgtc 3540
 181 cctctgtaga tagaaacaag gggagaaggg gaaaaaaaagt acttgttattt cttttgttcc 3600
 182 atggtggtgg tgggggtggg cggctcagcc tcgtgagtgc agtattggc aaaccggagg 3660
 183 ctgcggcaac ctgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
 184 caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaaa 3776
 186 <210> SEQ ID NO: 4
 187 <211> LENGTH: 1148
 188 <212> TYPE: PRT
 189 <213> ORGANISM: Zea mays
 191 <400> SEQUENCE: 4
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 195 Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
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 198 Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
 199 35 40 45
 201 Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
 202 50 55 60
 204 Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
 205 65 70 75 80
 207 Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
 208 85 90 95
 210 Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
 211 100 105 110
 213 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
 214 115 120 125
 216 Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
 217 130 135 140
 219 Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
 220 145 150 155 160
 222 Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
 223 165 170 175
 225 Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
 226 180 185 190
 228 Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
 229 195 200 205
 231 Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
 232 210 215 220
 234 Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
 235 225 230 235 240
 237 Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
 238 245 250 255
 240 Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
 241 260 265 270
 243 Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln

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246	Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp		
247	290	295	300
249	Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg		
250	305	310	315
252	Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile		320
253	325	330	335
255	Ile Ile Arg Leu Val Val Leu Cys Phe Phe His Tyr Arg Val Met		
256	340	345	350
258	His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys		
259	355	360	365
261	Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp		
262	370	375	380
264	Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe		
265	385	390	395
267	Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Val		400
268	405	410	415
270	Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr		
271	420	425	430
273	Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys		
274	435	440	445
276	Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser		
277	450	455	460
279	Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr		
280	465	470	475
282	Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp		480
283	485	490	495
285	Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala		
286	500	505	510
288	Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val		
289	515	520	525
291	Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly		
292	530	535	540
294	Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln		
295	545	550	555
297	Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu		560
298	565	570	575
300	Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His		
301	580	585	590
303	His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val		
304	595	600	605
306	Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile		
307	610	615	620
309	Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro		
310	625	630	635
312	Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp		640
313	645	650	655
315	Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe		
316	660	665	670

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 201

Seq#:19; N Pos. 262

Seq#:20; Xaa Pos. 88